Ribonucleotide Reductase Large Subunit (RRM1) Gene Expression May Predict Efficacy of Adjuvant Mitotane in Adrenocortical Cancer.

RIBONUCLEOTIDE REDUCTASE LARGE SUBUNIT (RRM1) GENE EXPRESSION MAY PREDICT EFFICACY OF ADJUVANT MITOTANE IN ADRENOCORTICAL CANCER.

Marco Volante, Massimo Terzolo, *Martin Fassnacht, Ida Rapa, Antonina Germano, *Silviu Sbiera, Fulvia Daffara, Paola Sperone, Giorgio Scagliotti, *Bruno Allolio, Mauro Papotti, Alfredo Berruti.

Department of Clinical and Biological Sciences, University of Turin, San Luigi Hospital, Orbassano, Turin, Italy; *Department of Medicine I, University Hospital Wurzburg, Wurzburg, Germany

Work supported by grants from the Italian Association for Cancer Research (AIRC, Milan, grant no. IG/10795/2010 to MP), from the Regione Piemonte (Progetto Ricerca Sanitaria Finalizzata, D.G.R. n. 35-4231 dated 06.11.2006 to MV, and Ricerca Sanitaria Finalizzata 2008 to AB), from the Italian Ministry of University and Scientific and Technological Research (PRIN, grant n° 20085P5S49 to MT), the Deutsche Krebshilfe (grant # 107111 to MF), and the German Research Foundation DFG (grant # FA 466/3-1 to M.F.).

Address for correspondence:

Alfredo Berruti MD, Department of Clinical and Biological Sciences at San Luigi Hospital, University of Turin, Division of Medical Oncology, Regione Gonzole 10, 10043 Orbassano, Torino, Italy; Phone: +390119026512; Fax: +390119026992; Email: alfredo.berruti@gmail.com

Runnig head: RRM1 and mitotane in adrenal cancer

The present study has been presented in part at the 3rd International Adrenal Cancer Symposium, Wurzburg, Germany, February 17-19, 2011

Abstract

PURPOSE. Mitotane is the most broadly used systemic therapy for adrenocortical carcinoma (ACC), but its mechanism of action and possible predictors of treatment response are currently poorly defined. Our aim was to evaluate the gene expression of ribonucleotide reductase large subunit 1 (RRM1) and excision repair cross-complementation group 1 (ERCC1) in ACC as potential biomarkers for clinical outcome and response to mitotane.

EXPERIMENTAL DESIGN. Forty-five and 47 tissue samples from two cohorts (Orbassano, Italy; Wuerzburg, Germany) of completely resected ACC were centrally analyzed using Real Time PCR for RRM1 and ERCC1 expression. Fifty-four patients received surgery alone and 38 received adjuvant mitotane after surgery. Clinical and pathological features were highly comparable in the two series. H295R and SW-13 ACC cell lines were also used for pharmacological tests.

RESULTS. ERCC1 gene expression was not associated to clinical outcome. In contrast, high RRM1 gene expression was associated to shorter disease-free and overall survival at both univariate and multivariate analysis. In patients with low RRM1 gene expression adjuvant mitotane was associated with improved disease free survival, whereas this effect was lost in cases with high RMM1 expression. In vitro mitotane induced strong up-regulation of RRM1 transcription (up to 25-fold increase) in mitotane-insensitive SW-13 but not in mitotane-sensitive H295R cells. Furthermore, RRM1 silencing in SW-13 cells induced sensitivity to mitotane.

CONCLUSION. Our *in vitro* and *in vivo* data indicate that RRM1 gene expression is functionally associated to mitotane sensitivity and support a possible role of RRM1

determination as a novel molecular biomarker predicting response to adjuvant mitotane in ACC.

KEY WORDS: adrenocortical carcinoma, RMM1, predictive marker, mitotane

Translational relevance

Mitotane is the reference drug in the management of adrenocortical carcinoma (ACC) and is increasingly prescribed in an adjuvant setting. Serum mitotane levels are the only known predictive factor of efficacy. In the present paper, we observed in two independent series of radically resected ACC patients, that in patients with low ribonucleotide reductase large subunit 1 (RRM1) gene expression adjuvant mitotane was associated with improved disease free survival, whereas this effect was lost in cases with high RMM1 expression. Moreover, this observation was supported by data in adrenal cancer cell lines demonstrating that low responsiveness to mitotane was associated to up-modulation of RRM1 gene and that selective RRM1 silencing can restore mitotane sensitivity *in vitro*. The present data are of translational relevance since they generate the hypothesis that RRM1 gene expression is a genetic marker predicting mitotane efficacy that may be used to select patients who can benefit from adjuvant mitotane therapy.

Introduction

Adrenocortical carcinoma (ACC) is a rare and aggressive malignant tumor.[1-2] Surgery is the mainstay of therapy,[3-4] however medical treatment has also an important role because a large proportion of ACC patients presents with metastatic disease and most of the radically resected patients relapse after surgery, often with metastases.[5] Mitotane, either as monotherapy or in combination with cytotoxic chemotherapy, is the reference drug in the management of advanced ACC.[6-7]

Mitotane has also been used in an adjuvant setting. A large retrospective multicentric study performed at several referral centers in Italy and Germany has shown that adjuvant mitotane therapy prolonged recurrence-free and overall survival in radically resected ACC patients[8] and a panel of international experts recently recommended the administration of adjuvant mitotane in all patients at high risk of relapse.[9] However, this recommendation based on retrospective data has a low level of evidence, whereas a prospective randomized controlled trial on adiuvant mitotane treatment is currently under way (www.adiuvo-trial.org).

The risk of relapse or death in ACC patients may be assessed by several parameters, including pathological features, such as mitotic index,[10-12] molecular alterations, such as TP53 mutations and beta-catenin dysregulation,[13] or immunohistochemical markers including matrix metalloproteinase type 2 (MMP-2),[14] glucose transporter 1 (GLUT1)[15] and steroidogenic factor-1 (SF-1).[16] In addition, a gene signature profile has been shown to correlate more closely with prognosis than clinical data.[17,18] However, in contrast to the availability of prognostic parameters, very few factors predicting the efficacy of treatment have been identified. A single study reported that a low immunohistochemical expression of excision repair cross-complementation group 1 (ERCC1) correlated to objective

response and overall survival in ACC patients treated with platinum-based chemotherapy.[19] Concerning mitotane treatment, attainment of drug levels in the target range of 14-20 mg/L is the only factor predicting efficacy that has been convincingly demonstrated.[20-22]

Since most ACC patients are at high risk of recurrence after primary surgery applying current prognostication methods,[9] selection of patients for adjuvant therapy with mitotane based upon predictive factors for drug efficacy may represent a superior approach than selection based on prognostic markers. Such an approach is particularly appealing because mitotane therapy is a cumbersome and quite toxic treatment, that has to be maintained for years and needs frequent drug monitoring and a complex regimen of steroid replacement and management of adverse events.[5,23]

We designed the present study stemming from the previous work of our research group on the role of genes involved in DNA repair or synthesis as predictors of response to chemotherapy in non-small cell lung cancer, neuroendocrine tumors and mesothelioma[24-26] and aimed to test the expression of ribonucleotide reductase large subunit 1 (RRM1) and ERCC1 genes in a cohort of ACC patients and to correlate gene expression with clinical outcome. The rationale for investigating RRM1 and ERCC1 genes as potential biomarker in ACC was based on their prognostic relevance in other cancer types[27] and on the sequential use of platinum and gemcitabine-based therapy in ACC.[28] In addition, we analyzed the predictive role of these two markers in patients treated with adjuvant mitotane and strengthened the *in vivo* results by *in vitro* analysis on ACC cell lines.

Patients and methods

Patients. Ninety-two patients with ACC radically resected between 1989 and 2007 at the University of Turin at Orbassano (Turin), Italy (45 patients) and 35 centers in Germany all coordinated by the German ACC Registry (47 patients) were included according to the following: 1) age of 18 years or older; 2) histologically confirmed diagnosis of ACC after revision (MV, MP); 3) stage I to III disease, 4) complete tumor resection, 5) availability of follow-up information, 6) availability of representative paraffin-embedded tissue block(s). All patients fulfilling the inclusion criteria were included in the study. All German patients, during follow-up were transferred to the center in Würzburg. The diagnosis of ACC was based on established clinical and biochemical parameters[29] and the pathological Weiss score[30]. Parameters recorded included age, sex, hormone secretion (according to ENSAT recommendations at www.ensat.org/acc.htm), ENSAT stage at diagnosis,[31] initial therapeutic options including primary surgery, disease-free survival (DFS), defined by the time elapsing from diagnosis to either disease relapse or patient death, overall survival (OS), calculated from diagnosis till death, Weiss score, mitotic count, sites of metastases at the time of progression. Relapse was ascertained by computerized tomography (or magnetic resonance imaging) of chest and abdomen every 3-6 months. Disease relapse was defined as the appearance during follow-up of local recurrence or metastatic disease at imaging techniques. Adjuvant mitotane was offered to patients considered at high risk of relapse, in presence of the following criteria: 1) stage III ACC; 2) high mitotic index (the value of mitotic index prompting treatment ranged between 10 and 20 mitoses per 50 HPF among centers). When a post-operative adjunctive measure was deemed necessary, a monitored mitotane treatment aiming at plasma concentrations between 14 and 20 mg/l,[20,21] was employed. In the absence of intolerability to mitotane, treatment was scheduled for at least 2 years, or till ACC recurrence. All the patients received the same mitotane formulation (Lysodren, 500 mg tablets) that was purchased by Bristol-Meyers Squibb, USA, till 2003

and thereafter by Laboratoire HRA Pharma, France. Mitotane was given orally starting with 1-2 g daily followed by progressive dose increments according to local protocols and patient compliance with the aim to reach concentrations between 14–20 mg/l. When such or even higher concentrations were attained, doses were tapered with further individual dose adjustments guided by the results of mitotane measurement and toxicity assessment. In the event of unacceptable side effects, the patients were allowed to return to a lower dose or discontinue mitotane temporarily restarting with a lower dose. Follow-up protocols were similar among the different centers including imaging of both chest and abdomen at baseline and thereafter every 3-6 months until disease progression or end of the study period. Follow-up procedures did not vary according to whether the patients received adjuvant mitotane or not. At each visit, the patients underwent physical examination, routine laboratory evaluation and hormonal work-up. Monitoring of mitotane concentrations was done in treated patients. For recurrent disease, radical surgery was performed if complete resection seemed feasible. In case of not resectable disease, mitotane naïve patients were treated with mitotane alone or in combination with cytotoxic drugs. In patients with recurrence during mitotane treatment, chemotherapy was added. Patients gave informed consent for collecting tissue and clinical data, and the study was approved by the ethics committees of both centres.

Cell culture, siRNAs and pharmacological assays. NCI-H295R and SW-13 cell lines were supplied from the American Type Culture Collection (ATCC, Rockville, MD, USA). The H295R cells were cultured in a 1:1 mixture of Dulbecco's Modified Eagle's Medium and Ham's F-12 Nutrient mixture (DMEM/F12) (Sigma, St. Louis, MO, USA) supplemented with 1% L- glutamine (Sigma, St. Louis, MO, Usa) and 2.5% of Nu-Serum (Becton Dickinson, San Jose, CA), and enriched with 1% of ITS+Premix (Becton Dickinson, San Jose, CA);

whereas SW-13 cells were cultured in DMEM (Sigma) supplemented with 10% fetal bovine serum (ATCC). Three human non-small cell lung cancer cell lines (two from adenocarcinoma - NCI-H520 and NCI-H1395, and one from squamous cell carcinoma - SKMES), also purchased from ATCC, were used as controls; all cells were maintained in RPMI-1640 medium, supplemented with 10% FCS, 2mM L-glutamine, penicillin (25 units/ml) and streptomycin (25 µg/ml, all from Sigma-Aldrich, St. Louis, MO, USA). For RRM1 silencing experiments in SW-13 cells, on-Target plus Smart Pool siRNAs targeting RRM1, on-Target plus Smart Pool siRNAs non-targeting and Siglo-Transfection indicator siRNA were used (Dharmacon® CO, USA). Interferin siRNA transfection reagent was purchased from Polyplus transfection (NY, USA). Transfection of SW-13 was first optimized by measuring the level of Siglo-green transfection indicator introduced with Interferin™, by flow cytometry using FACS Canto II (Becton Dickinson, San Jose, CA). Briefly, using a reverse transfection, siRNAs (at a final concentration of 100nM) and Interferin were diluted in DMEM without serum, and incubated for 10 min at room temperature. Lipoplexes were then transferred to multi-well tissue culture plates and, overlaid with $25x10^4$ cells/well. After 24 h (cultured overnight), the medium was changed, and the cells were then cultured in medium alone (basal) or in medium containing different concentrations (1; 5; 10; 25; 50; 100 µM) of mitotane (Supelco, Sigma; dissolved in 100% methanol, Sigma), for 48h (SW-13) or 72h (H295R). These concentrations are in a range comparable to those reached in plasma levels in vivo. Cell viability was measured using WST-1 reagent (Roche Applied Science, Penzberg, Germany) following the supplied protocol.

RNA isolation from paraffin embedded tissues and cell lines. Representative tumour areas were dissected under stereomicroscopic assistance from 10 µm sections of paraffin-

embedded tissue in RNAse-free conditions. RNA isolation was performed by commercially available RNA extraction kits designed for paraffin material according to the manufacturer's instructions (High Pure RNA Paraffin Kit; Roche Applied Science, Milano, Italy). Four samples of normal paraffin embedded adrenal tissue collected from 1 to 10 year-old blocks were also analyzed in parallel and compared to a cDNA obtained from a commercial total RNA (Stratagene, La Jolla, CA). Total RNA from cell lines lysates was extracted using QIAzol lysis Reagent (Qiagen, Tokyo, Japan). Complementary DNA was transcripted using 500µg/ml oligodT (Roche Applied Science, Penzberg, Germany) and 500M-MLV RT (200U/µl) (Invitrogen, Carlsbad, California) according to standard protocols.

Quantitative real time PCR. Relative cDNA quantification for RRM1, ERCC1 and an internal reference gene (β-actin) was done in duplicate using a fluorescence-based real-time detection method (ABI PRISM 7900 Sequence Detection System - Taqman; Applied Biosystems, Foster City, CA) using primers and probes previously published.[26,32] To analyze target gene expression in individual tumors, the relative gene expression levels were expressed as ratios (differences between the Ct values) between two absolute measurements (genes of interest/internal reference gene). Then, the ΔΔCt values were calculated subtracting ΔCt values of each case to the value of the case with the lowest expression, and converting the ratio by the $2^{-\Delta\Delta Ct}$ formula; cases were considered of low or high expression according to the median expression level obtained.

Statistical analysis. Correlation between the expression of the two gene was tested using the Spearman's method, differences of categorical variables were analyzed using the chi-square test. DFS and OS survival curves were computed using the Kaplan-Meier method and compared using the log-rank test. Hazard ratios (HR) for disease progression and

patient death were estimated using the Cox proportional hazard model. Multivariate analyses were performed adjusting for patient age, sex, ACC stage, mitotic count, cortisol secretion. Cox models were also used to assess the presence of heterogeneity in the effect of marker expression in the different patient subgroups, defined by the covariates, by including in the model the appropriate treatment/covariate interaction term(s). *In vitro* efficacy of mitotane in non silenced and RRM1 siRNA SW-13 cells was measured by means of the F test. All p values reported are the result of two-sided tests. Statistical analyses were performed by using the SPSS for windows software (version 17).

Results

Patients. Both cohorts (**Table 1**) were comparable in terms of age, sex proportion, stage of disease, presence of clinical syndromes and tumor characteristics. Adjuvant mitotane therapy was administered to 18 Italian and 20 German patients, respectively; the remaining patients did not receive any post operative treatment. Target mitotane levels were reached in less than 40% of cases. The median follow-up was 66.3 months in all patients, and 80 and 62.8 months in the Italian and German cohorts, respectively. During follow-up, 29 patients of the Italian series (67.4%) and 35 of the German series (74.5%) developed disease recurrence while 28 (54.9%) and 23 (48.9%) patients, respectively, died of ACC progression. Mitotane treated patients had a longer DFS than patients followed up only: median 22.5 months [95% confidence interval (CI) 1.8-43.1] versus 13.2 months (95% CI: 6.2-20.2), Hazard Ratio (HR) 0.70 (95% CI 0.43-1.16, p=0.17), and longer overall survival; median 154 months (95% CI 65.1-242.9) versus 53 months (95% CI 22.6-83.4), HR 0.63 (95% CI: 0.34-1.16, p=0.14).

Correlation between RRM1 and ERCC1 gene expression levels and patient/tumor characteristics. ERCC1 gene expression in normal adrenal tissues was rather low as compared to a commercially available total RNA pool, whereas RRM1 gene expression levels were comparable to reference total RNA. Moreover, the difference in RRM1 gene expression levels among normal tissues collected from paraffin blocks of different ages was in the range of 1-fold change (**Figure 1**), therefore showing that the time-frame of sample collection did not influence gene expression analysis. RRM1 and ERCC1 gene expression levels were reciprocally correlated in the patients' study population (Spearman's correlation test: R; 0.4425, p=0.0021). When dichotomized at the median value, both genes did not show any significant relationship with pathological features, except for the higher RRM1 expression levels in cases with a high mitotic count ($\leq$10 as compared to >10 mitoses in 50HPF, p=0.035).

Relationship between RRM1 and ERCC1 gene expression and survival (**Table 2**). ERCC1 gene expression was not associated with DFS and OS neither at univariate nor multivariate analysis. Conversely, high RRM1 expression levels were associated with shorter DFS both in univariate [p<0.0001] and multivariate analysis [p=0.002]. Similar results were seen for overall survival [univariate: p<0.0001; multivariate: p<0.0001]. Dividing patients according to each population, the prognostic role of RRM1 was more evident in German series than the Italian series (interaction test p=0.079), but similar results have been obtained in the two series in terms of survival (interaction test p=0.99).

Relationship between RRM1/ERCC1 gene expression and outcome of adjuvant mitotane treatment. Patients attaining the target mitotane levels were similarly distributed between patients showing different RRM1 and ERCC1 expression. To test the predictive role of

RRM1 and ERCC1 gene expression in the adjuvant setting, patients treated with adjuvant mitotane or simply followed up were analyzed and stratified according to marker expression (dichotomised at the median value). In patients with low RRM1 expression, mitotane administration was associated with a significantly longer DFS than that of patients undergoing follow up only **(Figure 2)**. The prognostic role of adjuvant mitotane therapy in patients with low RRM1 expression was maintained in multivariate analysis after adjustment for sex, age, stage and mitosis status [HR of recurrence 0.31 (95% CI: 0.13-0.74); p=0.009], whereas no effect of mitotane treatment on DFS was observed in patients with high RRM1 levels [adjusted HR of recurrence 0.87 (95% CI: 0.43-1.79); p=0.72] (**Figure 2**); the interaction test was close to attain the statistical significance (p=0.098). The HRs of recurrence in mitotane-treated patients compared to untreated patients with low RRM1 expression did not vary in the two patient cohorts considered separately: HR 0.36 (95% CI: 0.12-1.14, p=0.08) in the Italian series and HR 0.40 (95% CI: 0.11-1.47, p=0.17) in the German series (interaction test: p=0.83). The relationship between the prognostic role for DFS of adjuvant mitotane therapy and RRM1 expression was also explored dividing patients according to tertile distribution of RRM1. A step wise increase in the HR of adjuvant mitotane vs follow-up was observed: HR 0.36, (95% CI: 0.12-1.09, p=0.07) in the 1st tertile, HR 0.47 (95% CI: 0.19-1.13, p=0.09) in the 2nd tertile and HR 1.33 (95% CI: 0.63-2.79, p=0.45) in the 3rd tertile. These HRs were significantly different at the interaction test (p=0.034). Conversely adjuvant mitotane failed to be associated with overall survival either in patients with low RRM1 or in those with high RRM1 **(figure 2)**, adjusted HR 0.50 (95% CI: 0.16-1.60, p=0.25) and 0.56 (95% CI: 0.25-1.29, p=0.17), interaction test (p=0.98). As far as as ERCC1 is concerned, adjuvant mitotane therapy failed to be significantly associated with DFS in patients with low or high ERCC1 expression **(figure 3)**, in multivariate analysis however adjuvant mitotane therapy

was significantly associated with lower risk of relapse HR 0.40 (95% CI: 0.18-0.90, p=0.026) in patients with low ERCC1 expression but not in those with high ERCC1 expression, HR 0.65 (95% CI: 0.31-1.37, p=0.26), these two HRs were not different at the interaction test (p=0.79). Overall survival of mitotane treated patients was not significantly different than patients followed up only either in patients with low ERCC1 expression **(figure 3)**, adjusted HR 0.47 (95% CI: 0.18-1.24, p=0.13) or in patients with high ERCC1 expression, adjusted HR 0.63 (95% CI: 0.26-1.51), interaction test (p=0.94).

RRM1 and ERCC1 modulation and interplay with mitotane responsiveness in vitro. The possible functional interaction between RRM1 and ERCC1 gene expression and mitotane responsiveness was tested *in vitro* in two established ACC cell line models, the H295R and SW-13 cells. Baseline ERCC1 gene expression was comparable in the two cell lines tested and was not modulated under mitotane administration (**supplemental Figure 1**). RRM1 gene expression levels were similar in H295R and SW-13 cells (data not shown). Mitotane treatment induced a dose-dependent reduction of H295R cell viability and the H295R cells did not show significant changes in their RRM1 gene expression levels. Conversely, SW-13 cell viability was unaffected by mitotane but SW-13 cells displayed an impressive increase in RRM1 gene expression levels (up to 25 times over baseline in cells incubated with 25μM mitotane) (**Figure 4**). By contrast, control non-small cell lung cancer cell lines were not sensitive to mitotane treatment nor showed significant up-modulation of RRM1 gene under mitotane treatment (**Figure 5**).

Thus, we inhibited RRM1 expression by RNA specific silencing (**Figure 6**). Efficiency of transfection measured by means of flow cytometry was optimal (not shown) and RRM1 mRNA expression in SW13 cells was knocked down by RRM1 siRNA to less than 10% of

control cells transfected with non-targeting siRNAs. Silencing of RRM1 gene in SW-13 did not affect cell viability under basal conditions but induced a mitotane sensitivity indicating a direct link between RRM1 gene expression and anti-proliferative activity of mitotane in this cell model.

Discussion

Mitotane is the reference drug for treatment of advanced ACC and is increasingly adopted in an adjuvant setting.[33-37] Demonstration of the adrenolytic effect of mitotane dates back to the fifties of the last century when studies demonstrated that administration of the drug was able to destroy the adrenal glands in animal models[38,39] and to inhibit steroidogenesis at different enzymatic steps.[23] However, the precise mechanism of action of mitotane remains still largely unknown, and it is generally thought that mitotane cytotoxicity is mediated through binding of the reactive acyl-chloride to mitochondrial proteins and subsequent oxidative damage through generation of free radicals.[23,37] Recently, mitotane has been shown to sensitize H295R and SW-13 ACC cells to ionizing radiations by attenuating DNA repair and interfering with cell proliferation,[40] data suggesting that mitotane, in addition to the assumed binding to proteins and phospholipids, may interact also with DNA, as was previously demonstrated *in vitro*.[41] Moreover, it is known that metabolic activation is required for mitotane biological activity,[37] but its metabolic pathway and the effective role of its metabolites, as well as its target molecules in tumor cells are far from being identified.

For the first time, in the present study we provide *in vitro* and *in vivo* evidence of a relationship between RRM1 enzyme and the antineoplastic activity of mitotane in ACC. RRM1 is an enzyme involved in the synthesis of deoxyribonucleotides for DNA synthesis and represents the cellular target for gemcitabine, being its mRNA expression and genetic

variants predictive of response to gemcitabine treatment in patients with different types of cancer.[27]

The present study includes two independent series of radically resected ACC patients recruited in two European countries.[35] In the overall patient population, low RRM1 gene expression was significantly associated to longer disease-free and overall survival and this contrasts with other tumor models, such as non-small cell lung cancer, where low RRM1 expression in patients treated with surgery is associated with reduced survival, whereas improved survival is observed in metastatic disease in gemcitabine-treated patients.[42] However, it should be noted that RRM1 may not be a direct target of mitotane and possible alternative molecular or metabolic interactions between mitotane and RRM1 are to be further evaluated to explain this apparent discrepancy. Moreover, *in vitro* analysis of control non-small cell lung cancer models showed that the anti-neoplastic mitotane efficacy as well as its effect in RRM1 gene modulation is specific for ACC cancer cell models (see also below). Subsequently, we tested if RRM1 gene expression affects the efficacy of adjuvant mitotane treatment, analyzing the DFS of patients treated with mitotane in the low and high RRM1 expression groups, respectively, in comparison to patients left untreated after surgery. Our results clearly indicate that mitotane efficacy was confined to the patients with low RRM1-expressing tumors, and this effect was evident also when the Italian and German cohorts were analyzed separately. Despite the significant DFS prolongation in patients with low RRM1 expressing tumors, mitotane therapy was not able to significantly influence the overall survival. Survival is affected by therapies administered upon progression and patients not receiving mitotane therapy in adjuvant setting received the drug at disease relapse, and this could have influenced the overall survival.

These data suggested a predictive role of RRM1 gene expression of mitotane efficacy in ACC and prompted a subsequent *in vitro* investigation in order to assess possible functional pharmacological interactions. Two established ACC cell lines were, therefore, analyzed for RRM1 gene expression levels at baseline and under mitotane treatment. Mitotane sensitivity in H295R cells was associated with a lack of RRM1 gene modulation, whereas SW-13 cells were not sensitive even at high doses of mitotane showing a significant and dose-dependent increase in RRM1 transcription following mitotane treatment. This observation was consistent with the data we obtained *in vivo* and supports the hypothesis that high RRM1 expression might impair the anti-neoplastic activity of mitotane. As a further step to establish a direct relationship between RRM1 and mitotane, RRM1 silencing was performed which sensitized SW-13 cells to mitotane, thus demonstrating that low RRM1 expression is of critical importance for mitotane antitumor efficacy. The lack of available tumor specimens sampled after mitotane treatment in the patient cohort prevented a subsequent tissue analysis to speculate the modulation of RRM1 *in vivo*; therefore the issue whether baseline RRM1 gene expression levels or rather its up-modulation under treatment are predictive of response to mitotane remains to be ascertained.

ERCC1 gene expression levels were neither prognostic nor predictive of response to mitotane in our study population. The trend to significance of greater efficacy of mitotane treatment in patients with low ERCC1 expression is, in our opinion, most probably justified by the significant correlation between RRM1 and ERCC1 gene expression levels.

Our study has certainly limitations and strengths. The retrospective nature of the study, the absence of randomization between mitotane treated and non treated patients and apparently relative small sample size might lead to unknown biases. However, when compared with the literature, our cohort seems to be quite representative for patients with

stage I-III ACC and we believe - acknowledging the rarity of the disease – that the sample size is one of the strength of this study. Moreover, the inclusion of two independent cohorts from different countries favors the generalization of the present results . Although it might be surprising that less than half of the patients have been treated with mitotane in this cohort,. this may be explained by the fact that more than 80% of patients had surgery before the results of our adjuvant mitotane study have been published.[43] Another strength of this study is the consistency of data on human tumors and cell culture *in vitro* experiments, providing new data that may help understanding the mechanism of action of mitotane and its target molecules.

In conclusion, the present data represent the first evidence that RRM1 gene expression levels predict response to mitotane treatment in an adjuvant setting and are functionally associated to mitotane sensitivity. These findings suggest that the determination of RRM1 gene expression may be of potential clinical utility to select patients for adjuvant mitotane therapy.

References

1. Balasubramaniam S, Fojo T: Practical considerations in the evaluation and management of adrenocortical cancer. Semin Oncol 2010; 37:619-626.

2. Volante M, Buttigliero C, Greco E, Berruti A, Papotti M. Pathological and molecular features of adrenocortical carcinoma: an update. J Clin Pathol 2008: 61:787-793.

3. Brix D, Allolio B, Fenske W, Agha A, Dralle H, Jurowich C, et al: Laparoscopic versus open adrenalectomy for adrenocortical carcinoma: surgical and oncologic outcome in 152 patients. Eur Urol 2010; 58: 609-615.

4. Porpiglia F, Fiori C, Daffara F, Zaggia B, Bollito E, Volante M, et al: Retrospective evaluation of the outcome of open versus laparoscopic adrenalectomy for stage I and II adrenocortical cancer. Eur Urol 2010; 57: 873-878.

5. Terzolo M, Berruti A: Adjunctive treatment of adrenocortical carcinoma. Curr Opin Endocrinol Diabetes Obes 2008; 15: 221-226.

6. Berruti A, Terzolo M, Sperone P, Pia A, Della Casa S, Gross DJ, Carnaghi C et al: Etoposide, doxorubicin and cisplatin plus mitotane in the treatment of advanced adrenocortical carcinoma: a large prospective phase II trial. Endocr Relat Cancer 2005; 12: 657-666.

7. Malandrino P, Al Ghuzlan A, Castaing M, Young J, Caillou B, Travagli JP, et al: Prognostic markers of survival after combined mitotane- and platinum-based chemotherapy in metastatic adrenocortical carcinoma. Endocr Relat Cancer 2010; 17: 797-807.

8. Terzolo M, Angeli A, Fassnacht M, Daffara F, Tauchmanova L, Conton PA et al: Adjuvant mitotane treatment for adrenocortical carcinoma. N Engl J Med 2007; 356:2372-2380.

9. Berruti A, Fassnacht M, Baudin E, Hammer G, Haak H, Leboulleux S, et al: Adjuvant therapy in patients with adrenocortical carcinoma: a position of an international panel. J Clin Oncol 2010; 28: e401-402.

10. Assié G, Antoni G, Tissier F, Caillou B, Abiven G, Gicquel C, et al: Prognostic parameters of metastatic adrenocortical carcinoma. J Clin Endocrinol Metab 2007; 92:148-154.

11. Volante M, Bollito E, Sperone P, Tavaglione V, Daffara F, Porpiglia F, et al: Clinicopathological study of a series of 92 adrenocortical carcinomas: from a proposal of simplified diagnostic algorithm to prognostic stratification. Histopathology 2009; 55: 535-543.

12. Giordano TJ. The argument for mitotic rate-based grading for the prognostication of adrenocortical carcinoma. Am J Surg Pathol 2011; 35: 471-473.

13. Ragazzon B, Libé R, Gaujoux S, Assié G, Fratticci A, Launay P, et al: Transcriptome analysis reveals that p53 and {beta}-catenin alterations occur in a group of aggressive adrenocortical cancers. Cancer Res 2010; 70: 8276-8281.

14. Volante M, Sperone P, Bollito E, Frangipane E, Rosas R, Daffara F et al: Matrix metalloproteinase type 2 expression in malignant adrenocortical tumors: Diagnostic and prognostic significance in a series of 50 adrenocortical carcinomas. Mod Pathol 2006; 19:1563-1569.

15. Fenske W, Völker HU, Adam P, Hahner S, Johanssen S, Wortmann S, et al: Glucose transporter GLUT1 expression is an stage-independent predictor of clinical outcome in adrenocortical carcinoma. Endocr Relat Cancer 2009; 16: 919-928.

16. Sbiera S, Schmull S, Assie G, Voelker HU, Kraus L, Beyer M, et al: High diagnostic and prognostic value of steroidogenic factor-1 expression in adrenal tumors. J Clin Endocrinol Metab 2010; 95: E161-171.

17. de Reyniès A, Assié G, Rickman DS, Tissier F, Groussin L, René-Corail F, et al: Gene expression profiling reveals a new classification of adrenocortical tumors and identifies molecular predictors of malignancy and survival. J Clin Oncol 2009; 27:1108-1115.

18. Ragazzon B, Assié G, Bertherat J: Transcriptome analysis of adrenocortical cancers: from molecular classification to the identification of new treatments. Endocr Relat Cancer 2011; 18: R15-27.

19. Ronchi CL, Sbiera S, Kraus L, Wortmann S, Johanssen S, Adam P, et al: Expression of excision repair cross complementing group 1 and prognosis in adrenocortical carcinoma patients treated with platinum-based chemotherapy. Endocr Relat Cancer 2009; 16:907-918.

20. Haak HR, Hermans J, van de Velde CJ, Lentjes EG, Goslings BM, Fleuren GJ, et al: Optimal treatment of adrenocortical carcinoma with mitotane: results in a consecutive series of 96 patients. Br J Cancer 1994; 69:947-951.

21. Baudin E, Pellegriti G, Bonnay M, Penfornis A, Laplanche A, Vassal G, et al: Impact of monitoring plasma 1,1-dichlorodiphenildichloroethane (o,p'DDD) levels on the treatment of patients with adrenocortical carcinoma. Cancer 2001; 92: 1385-1392.

22. Hermsen IG, Fassnacht M, Terzolo M, Houterman S, den Hartigh J, Leboulleux S, et al: Plasma concentrations of o,p'DDD, o,p'DDA, and o,p'DDE as predictors of tumor response to mitotane in adrenocortical carcinoma: results of a retrospective ENS@T multicenter study. J Clin Endocrinol Metab 2011; 96:1844-1851.

23. Veytsman I, Nieman L, Fojo T. Management of endocrine manifestations and the use of mitotane as a chemotherapeutic agent for adrenocortical carcinoma. J Clin Oncol 2009; 27: 4619-4629.

24. Righi L, Papotti MG, Ceppi P, et al: Thymidylate synthase but not excision repair cross-complementation group 1 tumor expression predicts outcome in patients with

malignant pleural mesothelioma treated with pemetrexed-based chemotherapy. J Clin Oncol 2010; 28: 1534-1539.

25. Ceppi P, Volante M, Ferrero A, et al: Thymidylate synthase expression in gastroenteropancreatic and pulmonary neuroendocrine tumors. Clin Cancer Res 2008; 14:1059-1564.

26. Ceppi P, Volante M, Novello S, et al: ERCC1 and RRM1 gene expressions but not EGFR are predictive of shorter survival in advanced non-small-cell lung cancer treated with cisplatin and gemcitabine. Ann Oncol 2006; 17:1818-1825.

27. Jordheim LP, Sève P, Trédan O, et al: The ribonucleotide reductase large subunit (RRM1) as a predictive factor in patients with cancer. Lancet Oncol 2011; 12: 693-702.

28. Fassnacht M, Libé R, Kroiss M, Allolio B: Adrenocortical carcinoma: a clinician's update. Nat Rev Endocrinol 2011; 7:323-335.

29. Allolio B, Fassnacht M. Clinical review: Adrenocortical carcinoma: clinical update. J Clin Endocrinol Metab 2006; 91: 2027-2037.

30. Weiss LM, Medeiros LJ, and Vickery AL: Pathologic features of prognostic significance in adrenocortical carcinoma. Am J Surg Pathol 1989; 13:202-206.

31. Fassnacht M, Johanssen S, Quinkler M, et al: Limited prognostic value of the 2004 International Union Against Cancer staging classification for adrenocortical carcinoma: proposal for a Revised TNM Classification. Cancer 2009; 115:243-250.

32. Ceppi P, Volante M, Saviozzi S, et al: Squamous cell carcinoma of the lung compared with other histotypes shows higher messenger RNA and protein levels for thymidylate synthase. Cancer 2006; 107: 1589-1596.

33. Schteingart DE: Adjuvant mitotane therapy of adrenal cancer - use and controversy. N Engl J Med 2007; 356:2415-2418.

34. Terzolo M, Fassnacht M, Ciccone G, et al: Adjuvant mitotane for adrenocortical cancer--working through uncertainty. J Clin Endocrinol Metab 2009; 94:1879-1880.

35. Fassnacht M, Johanssen S, Fenske W, et al: Improved survival in patients with stage II adrenocortical carcinoma followed up prospectively by specialized centers. J Clin Endocrinol Metab 2010; 95: 4925-4932.

36. Wängberg B, Khorram-Manesh A, Jansson S, et al: The long-term survival in adrenocortical carcinoma with active surgical management and use of monitored mitotane. Endocr Relat Cancer 2010; 17:265-272.

37. Hahner S, Fassnacht M: Mitotane for adrenocortical carcinoma treatment. Curr Opin Investig Drugs 2005; 6:386-394.

38. Nelson AA, Woodard G: Severe adrenal cortical atrophy (cytotoxic) and hepatic damage produced in dogs by feeding 2,2-bis(parachlorophenyl)-1,1-dichloroethane (DDD or TDE). Arch Pathol 1949; 48: 387-394.

39. Vilar O, Tullner WW: Effects of o,p'DDD on histology and 17-hydroxycorticosteroid output of the dog adrenal cortex. Endocrinology 1959; 65:80-86.

40. Cerquetti L, Sampaoli C, Amendola D, et al: Mitotane sensitizes adrenocortical cancer cells to ionizing radiations by involvement of the cicli B1/CDK complex in G2 arrest and mismatch repair enzymes modulation. Int J Oncol 2010; 37: 493-501.

41. Lund BO, Bergman A, Brandt I: In vitro macromolecular binding of 2-(2-chlorophenyl)-2-(4-chlorophenyl)-1,1-dichloroethane (o,p'-DDD) in the mouse lung and liver. Chem Biol Interact 1989; 70: 63-72

42. Rosell R, Danenberg KD, Alberola V, et al: Ribonucleotide reductase messenger RNA expression and survival in gemcitabine/cisplatin-treated advanced non-small cell lung cancer patients. Clin Cancer Res 2004; 10: 1318–1325.

43. Sperone P, Ferrero A, Daffara F, Priola A, Zaggia B, Volante M, et al: Gemcitabine plus metronomic 5-fluorouracil or capecitabine as a second-/third-line chemotherapy in advanced adrenocortical carcinoma: a multicenter phase II study. Endocr Relat Cancer 2010; 17: 445-453.

Figure legends

Figure 1. RRM1 gene expression levels in samples of normal adrenal tissue stored for a variable period of time, as compared to a commercially available pool of total RNA.

Figure 2. Influence of adjuvant mitotane on disease-free and overall survival of ACC patient population segregated according to RRM1 expression levels, evaluated using the Kaplan Meier curve estimation and univariate survival analysis (log-rank test).

Figure 3. Influence of adjuvant mitotane on disease-free and overall survival of ACC patient population segregated according to ERCC1 expression levels, evaluated using the Kaplan Meier curve estimation and univariate survival analysis (log-rank test).

Figure 4. Mitotane responsiveness (upper panels) and RRM1 gene expression under mitotane treatment (lower panels) in ACC cancer cells. Three replicate wells were used to determine each data point of cell viability measurements; for simplicity, mitotane values are represented in the X axis of the logarithmic curve as the effective concentrations; NT: untreated cells, corresponding to reference (1 unit of fold change).

Figure 5. Mitotane responsiveness (left panels) and RRM1 gene expression under mitotane treatment (right panels) in non-small cell lung cancer cells. Three replicate wells were used to determine each data point of cell viability measurements; for simplicity, mitotane values are represented in the X axis of the logarithmic curve as the effective concentrations; NT: untreated cells, corresponding to reference (1 unit of fold change).

Figure 6. Influence of RRM1 gene expression levels on mitotane sensitivity. In mitotane-insensitive SW-13 cells, RRM1 RNA silencing (RRM1 siRNA) reduced target gene expression but did not influence cell viability in the absence of mitotane; by contrast, an increase in mitotane sensitivity was induced by RRM1 interference (F test comparing IC50 doses of RRM1 siRNA and non-targeting siRNA control cells); for simplicity, mitotane values are represented in the X axis of the logarithmic curve as the effective concentrations.

RRM1 gene expression
(Fold change as compared to b-actin)
0
1
2
3
4
5
6
7
Total RNA
(Stratagene)
normal adrenal
(4 yrs-old block)
normal adrenal
(10 yrs-old block)
normal adrenal
(2 yrs-old block)
normal adrenal
(1 yrs-old block)

Figure 1

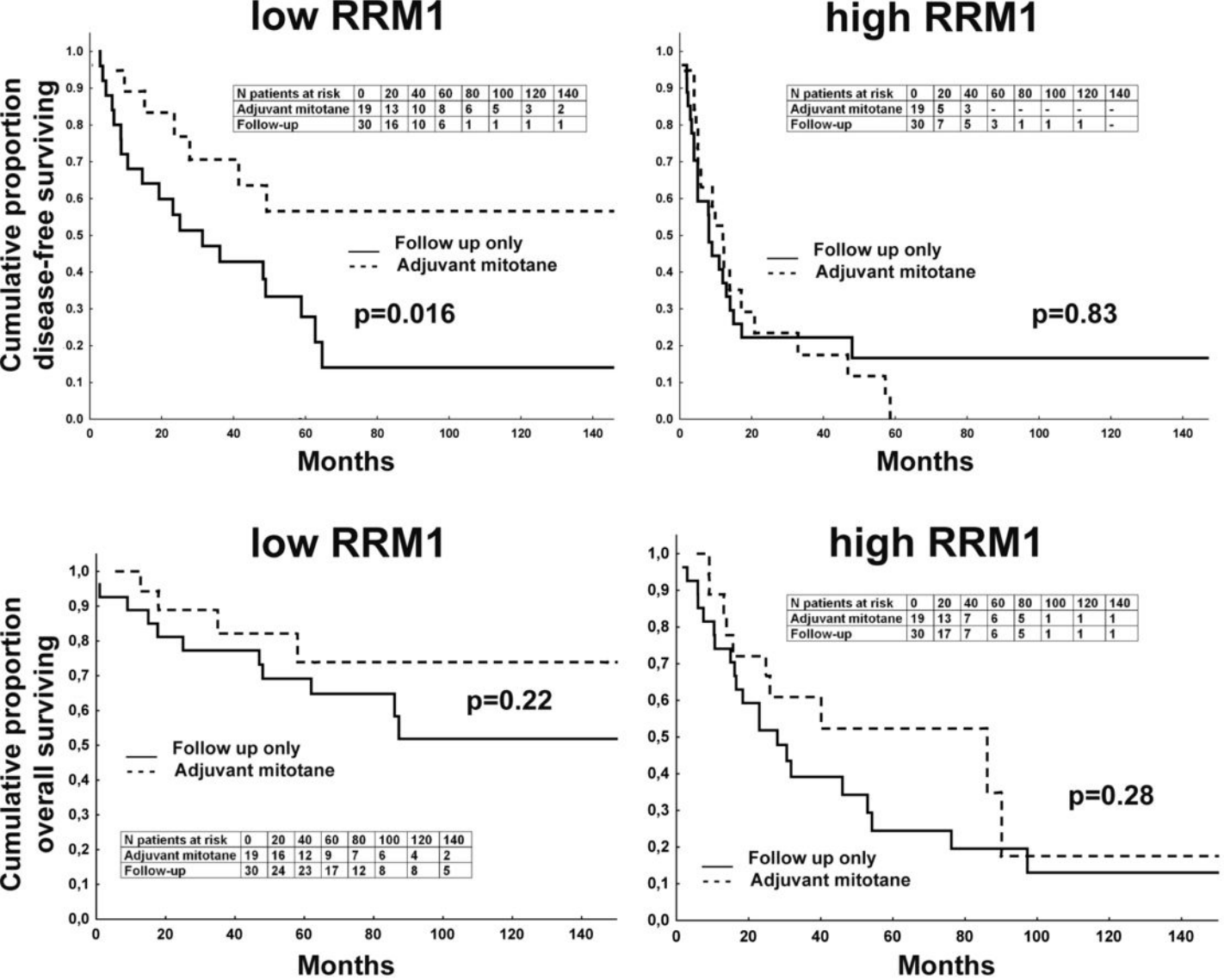
low RRM1
high RRM1
Cumulative proportion disease-free surviving
N patients at risk 0 20 40 60 80 100 120 140
Adjuvant mitotane 19 13 10 8 6 5 3 2
Follow-up 30 16 10 6 1 1 1 1
Follow up only
Adjuvant mitotane
p=0.016
N patients at risk 0 20 40 60 80 100 120 140
Adjuvant mitotane 19 5 3 - - - - -
Follow-up 30 7 5 3 1 1 1 -
Follow up only
Adjuvant mitotane
p=0.83
Months
low RRM1
high RRM1
Cumulative proportion overall surviving
p=0.22
Follow up only
Adjuvant mitotane
N patients at risk 0 20 40 60 80 100 120 140
Adjuvant mitotane 19 16 12 9 7 6 4 2
Follow-up 30 24 23 17 12 8 8 5
N patients at risk 0 20 40 60 80 100 120 140
Adjuvant mitotane 19 13 7 6 5 1 1 1
Follow-up 30 17 7 6 5 1 1 1
p=0.28
Follow up only
Adjuvant mitotane
Months

Figure 2

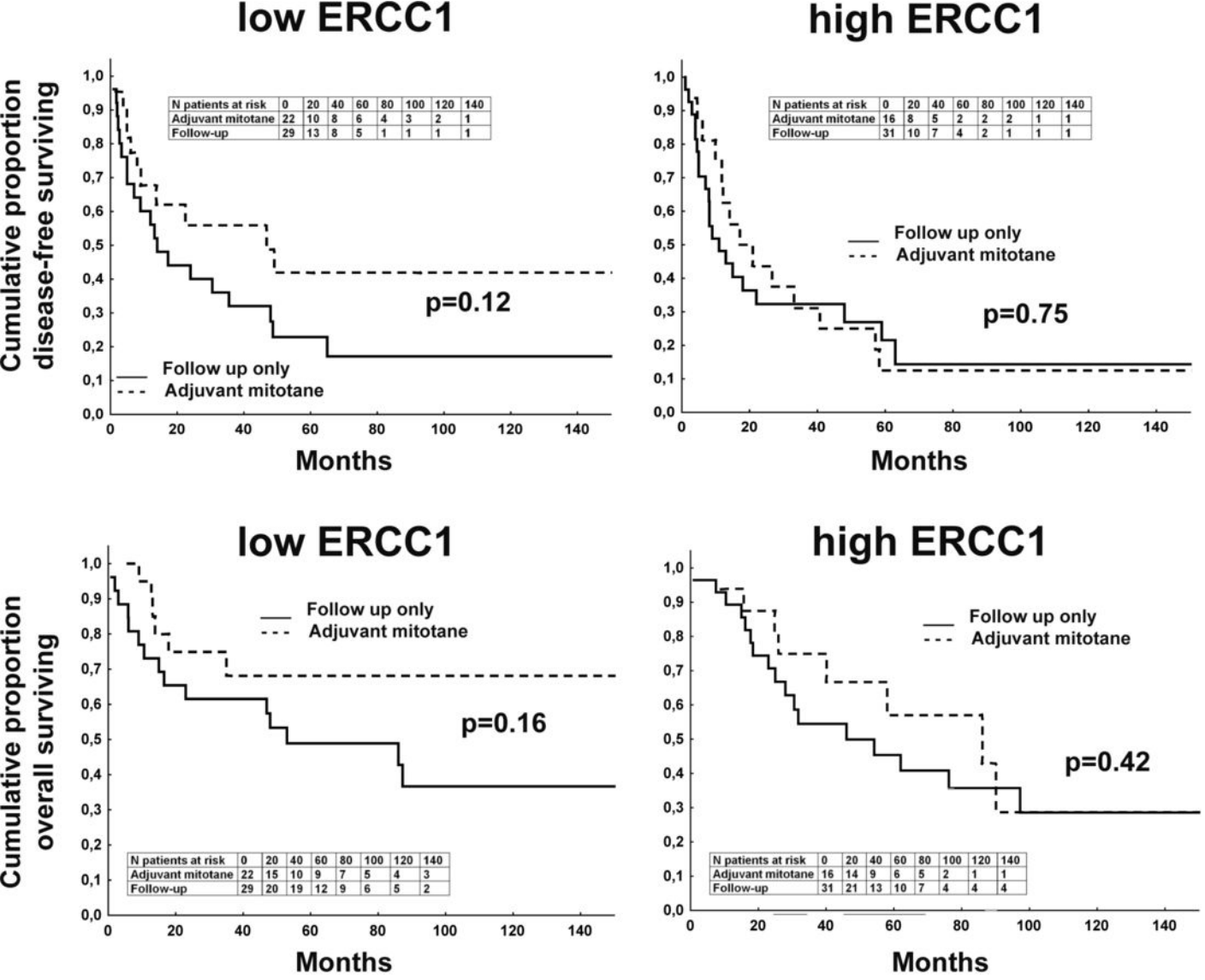
low ERCC1
high ERCC1
Cumulative proportion disease-free surviving
N patients at risk 0 20 40 60 80 100 120 140
Adjuvant mitotane 22 10 8 6 4 3 2 1
Follow-up 29 13 8 5 1 1 1 1
p=0.12
Follow up only
Adjuvant mitotane
Months
N patients at risk 0 20 40 60 80 100 120 140
Adjuvant mitotane 16 8 5 2 2 2 1 1
Follow-up 31 10 7 4 2 1 1 1
p=0.75
Follow up only
Adjuvant mitotane
Months
low ERCC1
high ERCC1
Cumulative proportion overall surviving
Follow up only
Adjuvant mitotane
p=0.16
N patients at risk 0 20 40 60 80 100 120 140
Adjuvant mitotane 22 15 10 9 7 5 4 3
Follow-up 29 20 19 12 9 6 5 2
Months
Follow up only
Adjuvant mitotane
p=0.42
N patients at risk 0 20 40 60 80 100 120 140
Adjuvant mitotane 16 14 9 6 5 2 1 1
Follow-up 31 21 13 10 7 4 4 4
Months

Figure 3

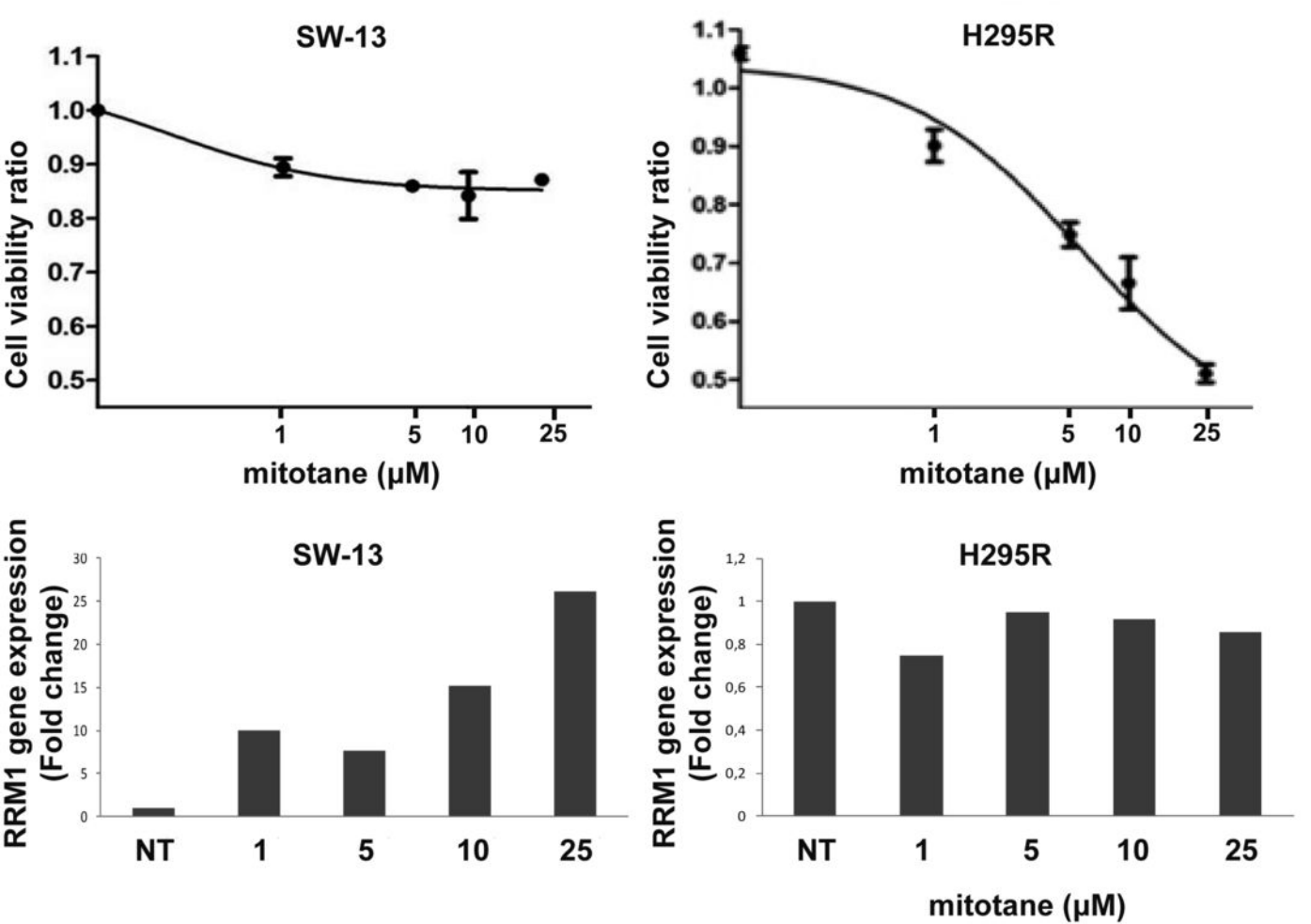
SW-13
Cell viability ratio
1.1
1.0
0.9
0.8
0.7
0.6
0.5
1
5
10
25
mitotane (µM)
H295R
Cell viability ratio
1.1
1.0
0.9
0.8
0.7
0.6
0.5
1
5
10
25
mitotane (µM)
SW-13
RRM1 gene expression (Fold change)
30
25
20
15
10
5
0
NT
1
5
10
25
H295R
RRM1 gene expression (Fold change)
1,2
1
0,8
0,6
0,4
0,2
0
NT
1
5
10
25
mitotane (µM)

Figure 4

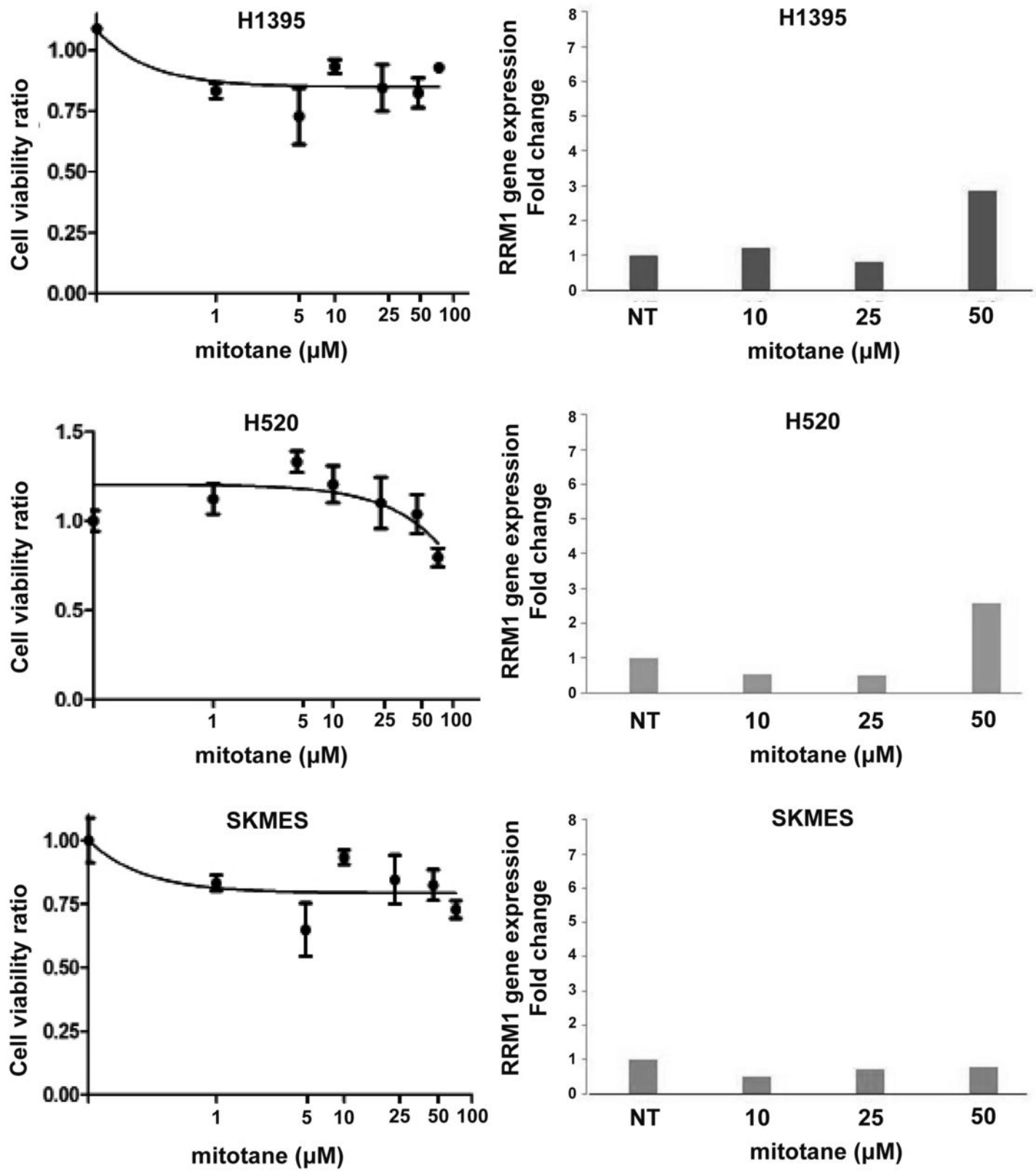
H1395
Cell viability ratio
1.00
0.75
0.50
0.25
0.00
1
5
10
25
50
100
mitotane (μM)
H1395
RRM1 gene expression
Fold change
8
7
6
5
4
3
2
1
0
NT
10
25
50
mitotane (μM)
H520
Cell viability ratio
1.5
1.0
0.5
0.0
1
5
10
25
50
100
mitotane (μM)
H520
RRM1 gene expression
Fold change
8
7
6
5
4
3
2
1
0
NT
10
25
50
mitotane (μM)
SKMES
Cell viability ratio
1.00
0.75
0.50
0.25
0.00
1
5
10
25
50
100
mitotane (μM)
SKMES
RRM1 gene expression
Fold change
8
7
6
5
4
3
2
1
0
NT
10
25
50
mitotane (μM)

Figure 5

SW-13 cells

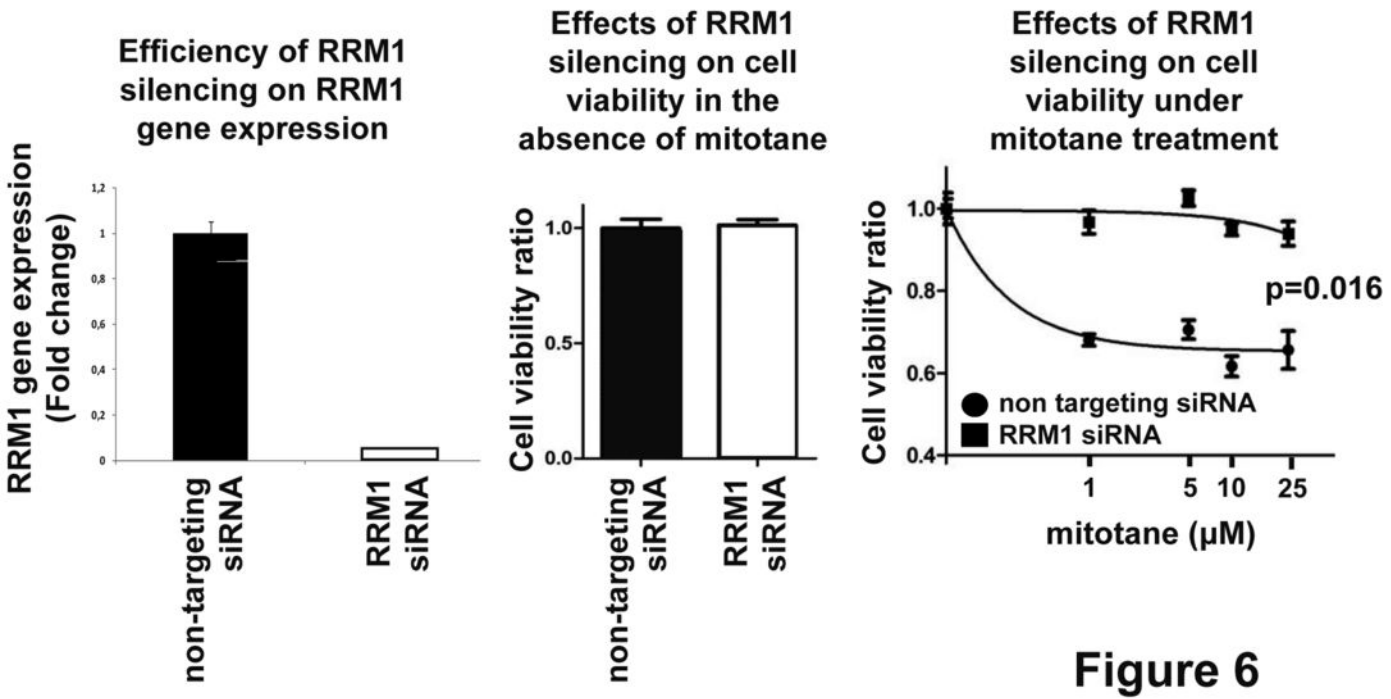

Figure 6

Table 1. Patients' characteristics

	Italian series	**German series**
No.	45	47
Age – yrs		
median (range)	46 (20-85)	49 (18-77)
Sex - No. (%)		
Male	20 (44.4%)	19 (40.4%)
Female	25 (55.6%)	28 (59.6%)
ENSAT Disease stage		
I	7 (15.6%)	4 (8.5%)
II	26 (57.8%)	23 (48.9%)
III	12 (26.6%)	20 (42.6%)
Secreting tumor - No. (%)		
Non-secreting tumor	22 (48.9%)	28 (59.6%)
Cortisol ± androgens	15 (33.3%)	12 (25.5%)
Androgens	4 (8.9%)	4 (8.5%)
Estradiol	-	3 (6.4%)
Mineralcorticoids	4 (8.9%)	-
Adjuvant mitotane - No. (%)		
Yes	18 (40.0%)	20 (42.5%)
No	27 (60.0%	27 (57.5%)
Patients with recurring ACC - No. (%)	29 (67.4%)	35 (74.5%)
Weiss score		
Median (range)	6 (4-9)	5 (3-9)
Mitoses in 50HPF - No. (%)		
≤5	12 (26.7%)	16 (34.0 %)
6-10	15 (33.3%)	6 (12.8%)
>10	18 (40.0%)	25 (53.2%)

Table 2. Prognostic role of ERCC1 and RMM1 expression in the series of 92 ACC.

	Univariate HR (95% CI)	**p**	**Multivariate HR (95% CI)**	**p**
Disease Free Survival				
High ERCC1	1.31 (0.81-2.13)	0.27	0.97 (0.57-1.64)	0.91
High RRM1	2.60 (1.57-4.30)	<0.0001	2.31 (1.36-3.95)	0.002
Overall Survival				
High ERCC1	1.25 (0.71-2.21)	0.44	0.98 (0.52-1.85)	0.96
High RRM1	3.19 (1.73-6.00)	<0.0001	3.59 (1.85-6.96)	<0.0001

ERCC1 and RRM1 expression was categorized at the median value.